



SEQUENCE LISTING

<110> THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
HUMAN SERVICES

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<120> Interferon Alpha Hybrids

<130> 4239-64129-01

<140> US 10/615,723

<141> 2003-07-08

<150> US 09/744,754

<151> 2001-01-24

<150> US 60/094,407

<151> 1998-07-28

<150> PCT/US99/15284

<151> 1999-07-06

<160> 44

<170> PatentIn version 3.1

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<223> Synthetic Oligonucleotide

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 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30
 aga cat gac ttt gga ttc ccc caa gag gag ttt gat ggc aac cag ttc 144
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60
 ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
 65 70 75 80
 ctc cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctg 288
 Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
 85 90 95
 gaa gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
 100 105 110
 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
 115 120 125
 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140
 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
 145 150 155 160
 agt tta aga agt aag gaa tg 500
 Ser Leu Arg Ser Lys Glu
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Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
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Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
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1				5					10					15		
ctc	ctg	gca	caa	atg	gga	aga	atc	tct	cct	ttc	tcc	tgc	ctg	aag	gac	96
Leu	Leu	Ala	Gln	Met	Gly	Arg	Ile	Ser	Pro	Phe	Ser	Cys	Leu	Lys	Asp	
			20					25					30			
aga	cat	gac	ttt	gga	ttc	ccc	cag	gag	gag	ttt	gat	ggc	aac	cag	ttc	144
Arg	His	Asp	Phe	Gly	Phe	Pro	Gln	Glu	Glu	Phe	Asp	Gly	Asn	Gln	Phe	
		35					40					45				
cag	aag	gct	caa	gcc	atc	tct	gtc	ctc	cat	gag	atg	atc	cag	cag	acc	192
Gln	Lys	Ala	Gln	Ala	Ile	Ser	Val	Leu	His	Glu	Met	Ile	Gln	Gln	Thr	
	50					55				60						
ttc	aat	ctc	ttc	agc	aca	aag	gac	tca	tct	gct	act	tgg	gaa	cag	agc	240
Phe	Asn	Leu	Phe	Ser	Thr	Lys	Asp	Ser	Ser	Ala	Thr	Trp	Glu	Gln	Ser	
65					70					75					80	
ctc	cta	gaa	aaa	ttt	tcc	act	gaa	ctt	aac	cag	cag	ctg	aat	gac	ctc	288
Leu	Leu	Glu	Lys	Phe	Ser	Thr	Glu	Leu	Asn	Gln	Gln	Leu	Asn	Asp	Leu	
				85					90					95		
gag	gcc	tgt	gtg	ata	cag	ggg	gtg	ggg	gtg	aca	gag	act	ccc	ctg	atg	336
Glu	Ala	Cys	Val	Ile	Gln	Gly	Val	Gly	Val	Thr	Glu	Thr	Pro	Leu	Met	
			100					105					110			
aag	gag	gac	tcc	att	ctg	gct	gtg	agg	aaa	tac	ttc	caa	aga	atc	act	384
Lys	Glu	Asp	Ser	Ile	Leu	Ala	Val	Arg	Lys	Tyr	Phe	Gln	Arg	Ile	Thr	
		115					120					125				
ctc	tat	ctg	aaa	gag	aag	aaa	tac	agc	cct	tgt	gcc	tgg	gaa	gtt	gtc	432
Leu	Tyr	Leu	Lys	Glu	Lys	Lys	Tyr	Ser	Pro	Cys	Ala	Trp	Glu	Val	Val	
	130					135					140					
aga	gca	gaa	atc	atg	aga	tct	ttt	tct	ttg	tca	aca	aac	ttg	caa	gaa	480
Arg	Ala	Glu	Ile	Met	Arg	Ser	Phe	Ser	Leu	Ser	Thr	Asn	Leu	Gln	Glu	
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agt	tta	aga	agt	aag	gaa	tg										500
Ser	Leu	Arg	Ser	Lys	Glu											
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<210> 11
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<400> 11

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
165

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<222> (1)..(495)

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1				5					10					15		

ctc	ctg	gca	cag	atg	agg	aga	atc	tct	ctt	ttc	tcc	tgc	ttg	aag	gac	96
Leu	Leu	Ala	Gln	Met	Arg	Arg	Ile	Ser	Leu	Phe	Ser	Cys	Leu	Lys	Asp	
		20					25						30			

aga	cgt	gac	ttt	gga	ttt	ccc	cag	gag	gag	ttt	ggc	aac	cag	ttc	caa	144
Arg	Arg	Asp	Phe	Gly	Phe	Pro	Gln	Glu	Glu	Phe	Gly	Asn	Gln	Phe	Gln	
		35					40					45				

aag	gct	gaa	acc	atc	cct	gtc	ctc	cat	gag	atg	atc	cag	cag	atc	ttc	192
Lys	Ala	Glu	Thr	Ile	Pro	Val	Leu	His	Glu	Met	Ile	Gln	Gln	Ile	Phe	
	50					55					60					

aat	ctc	ttc	agc	aca	aag	gac	tca	tct	gct	gct	tgg	gat	gag	acc	ctc	240
Asn	Leu	Phe	Ser	Thr	Lys	Asp	Ser	Ser	Ala	Ala	Trp	Asp	Glu	Thr	Leu	
65					70				75						80	

cta	gac	aaa	ttc	tac	act	gaa	ctc	tac	cag	cag	ctg	aat	gac	ctc	gag	288
Leu	Asp	Lys	Phe	Tyr	Thr	Glu	Leu	Tyr	Gln	Gln	Leu	Asn	Asp	Leu	Glu	
			85						90					95		

gcc	tgc	gtg	ata	cag	gag	gtt	ggg	gtg	gaa	gag	act	ccc	ctg	atg	aat	336
Ala	Cys	Val	Ile	Gln	Glu	Val	Gly	Val	Glu	Glu	Thr	Pro	Leu	Met	Asn	
			100				105						110			

gtg	gac	tcc	atc	ctg	gct	gtg	aag	aaa	tac	ttc	caa	aga	atc	act	ctt	384
Val	Asp	Ser	Ile	Leu	Ala	Val	Lys	Lys	Tyr	Phe	Gln	Arg	Ile	Thr	Leu	
		115					120					125				

tat	ctg	aca	gag	aag	aaa	tac	agc	cct	tgt	gcc	tgg	gag	gtt	gtc	aga	432
Tyr	Leu	Thr	Glu	Lys	Lys	Tyr	Ser	Pro	Cys	Ala	Trp	Glu	Val	Val	Arg	
	130					135					140					

gca	gaa	atc	atg	aga	tcc	ttc	tct	tta	tca	aaa	att	ttt	caa	gaa	aga	480
Ala	Glu	Ile	Met	Arg	Ser	Phe	Ser	Leu	Ser	Lys	Ile	Phe	Gln	Glu	Arg	
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tta	agg	agg	aag	gaa	tg											497
Leu	Arg	Arg	Lys	Glu												
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Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
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Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
20 25 30

Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
85 90 95

Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met Asn
100 105 110

Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr Leu
115 120 125

Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
130 135 140

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu Arg
145 150 155 160

Leu Arg Arg Lys Glu
165

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 <400> 15
 taggaggggc tcatcccaag cagc 24

<210> 16
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<210> 19

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 <210> 25
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 cagctgctgg ttgagttcag t 21

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gagctcgcat gctcatcatt ccttacttct taaact 36

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ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

ctc cta gaa aaa ttt tcc act gaa ctt aac cag cag ctg aat gac ctc 288
Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85 90 95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

agt tta aga agt aag gaa tg
 Ser Leu Arg Ser Lys Glu
 165

500

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Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
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Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
 65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
 145 150 155 160

Ser Leu Arg Ser Lys Glu

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 1 5 10 15

ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30

aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60

ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc 240
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
 65 70 75 80

ctc cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctc 288
 Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
 85 90 95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
 100 105 110

aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
 115 120 125

ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140

aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
 145 150 155 160

agt tta aga agt aag gaa tg
 Ser Leu Arg Ser Lys Glu
 165

500

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 <211> 166
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 <223> Gene Fusion

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Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
 1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
 65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
 145 150 155 160

Ser Leu Arg Ser Lys Glu
 165

<210> 33
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<400> 33
 tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata 48
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
 1 5 10 15
 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30
 aga cat gac ttt gga ttc ccc caa gag gag ttt gat ggc aac cag ttc 144
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60
 ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
 65 70 75 80
 ctc cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctg 288
 Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
 85 90 95
 gaa gcc tgc gtg ata cag gag gtt ggg gtg gaa gag act ccc ctg atg 336
 Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
 100 105 110
 aat gtg gac tcc atc ttg gct gtg aag aaa tac ttc caa aga atc act 384
 Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr
 115 120 125
 ctt tat ctg aca gag aag aaa tac agc cct tgt gct tgg gag gtt gtc 432
 Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140
 aga gca gaa atc atg aga tcc ttc tct tta tca aaa att ttt caa gaa 480
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu
 145 150 155 160
 aga tta agg agg aag gaa tg 500

Arg Leu Arg Arg Lys Glu
165

<210> 34
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Gene Fusion

<400> 34

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
100 105 110

Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu
145 150 155 160

Arg Leu Arg Arg Lys Glu
165

<210> 35
 <211> 500
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene Fusion

<220>
 <221> CDS
 <222> (1)..(498)

<400> 35
 tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata 48
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
 1 5 10 15
 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30
 aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60
 ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
 65 70 75 80
 ctc cta gaa aaa ttt tac act gaa ctt aac cag cag ctg aat gac ctc 288
 Leu Leu Glu Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
 85 90 95
 gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
 100 105 110
 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
 115 120 125
 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140
 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
 145 150 155 160
 agt tta aga agt aag gaa tg 500
 Ser Leu Arg Ser Lys Glu

165

<210> 36
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Gene Fusion

<400> 36

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

Leu Leu Glu Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
165

<210> 37
 <211> 500
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene Fusion

<220>
 <221> CDS
 <222> (1)..(498)

<400> 37
 tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata 48
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
 1 5 10 15
 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30
 aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60
 ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
 65 70 75 80
 ctc cta gaa aaa ttt tcc act gaa ctt tac cag cag ctg aat gac ctc 288
 Leu Leu Glu Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
 85 90 95
 gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
 100 105 110
 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
 115 120 125
 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140
 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
 145 150 155 160
 agt tta aga agt aag gaa tg 500
 Ser Leu Arg Ser Lys Glu
 165

<210> 38
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Gene Fusion

<400> 38

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
165

<210> 39

<211> 500
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene Fusion

<220>
 <221> CDS
 <222> (1)..(498)

<400> 39
 tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata 48
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
 1 5 10 15

ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30

aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60

ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc 240
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
 65 70 75 80

ctc cta gac aaa ttc tcc act gaa ctc tac cag cag ctg aat gac ctc 288
 Leu Leu Asp Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
 85 90 95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
 100 105 110

aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
 115 120 125

ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140

aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
 145 150 155 160

agt tta aga agt aag gaa tg 500
 Ser Leu Arg Ser Lys Glu
 165

<210> 40
 <211> 166
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Gene Fusion

<400> 40

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
 1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
 65 70 75 80

Leu Leu Asp Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
 145 150 155 160

Ser Leu Arg Ser Lys Glu
 165

<210> 41
 <211> 500

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene Fusion

<220>
 <221> CDS
 <222> (1)..(498)

<400> 41
 tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata 48
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
 1 5 10 15
 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30
 aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60
 ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc 240
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
 65 70 75 80
 ctc cta gac aaa ttc tac act gaa ctc aac cag cag ctg aat gac ctc 288
 Leu Leu Asp Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
 85 90 95
 gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
 100 105 110
 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
 115 120 125
 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140
 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
 145 150 155 160
 agt tta aga agt aag gaa tg 500
 Ser Leu Arg Ser Lys Glu
 165

<210> 42
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Gene Fusion

<400> 42

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
165

<210> 43
<211> 14
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> misc_feature

<222> (5)..(5)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (9)..(9)

<223> Xaa can be any naturally occurring amino acid

<400> 43

Leu Asp Lys Phe Xaa Thr Glu Leu Xaa Gln Gln Leu Asn Asp
1 5 10

<210> 44

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> misc_feature

<222> (5)..(5)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (9)..(9)

<223> Xaa can be any naturally occurring amino acid

<400> 44

Leu Glu Lys Phe Xaa Thr Glu Leu Xaa Gln Gln Leu Asn Asp
1 5 10